

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 103042

TO: Vanessa L Ford

Location: cm1/8d17/8e12

Art Unit: 1645

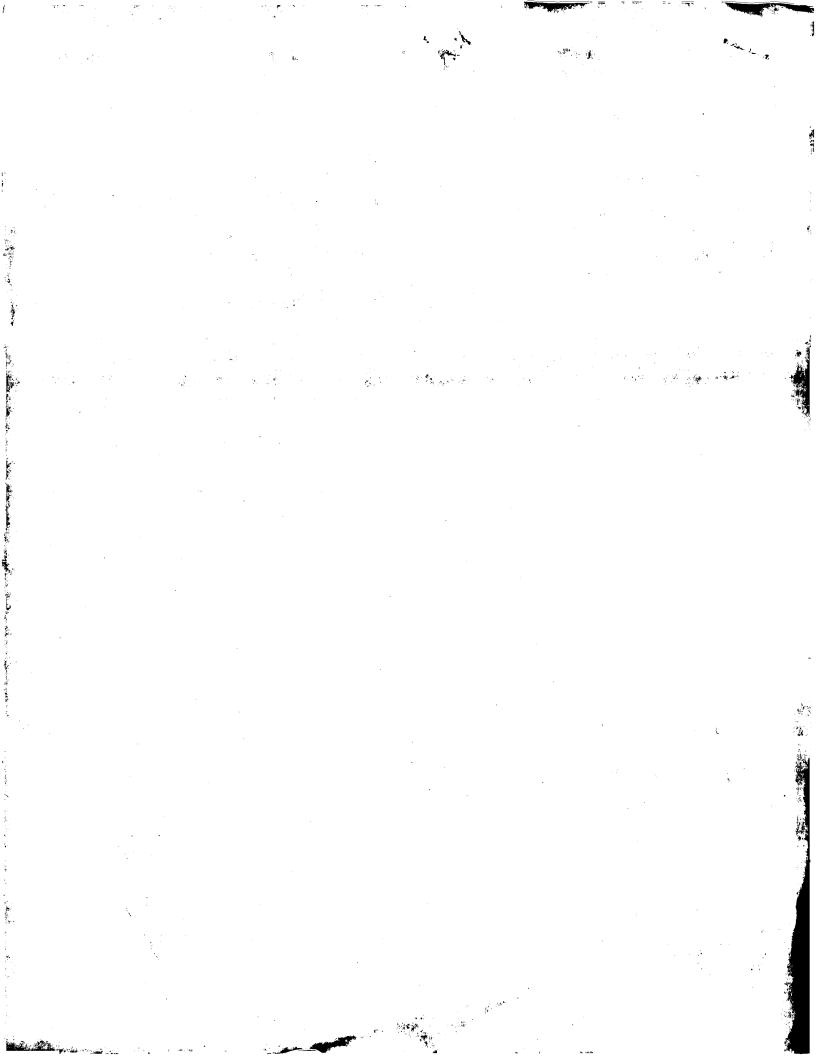
<u>Sept 7</u>, 2003

Case Serial Number: 10054354

From: P. Sheppard Location: CM1-1E03 Phone: (703) 308-4499

sheppard@uspto.gov

Search Notes		
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STIC-Biotech/ChemLib

Chan, Christina

Sent: To: Subject:

From:

Thursday, September 04, 2003 8:43 AM Ford, Vanessa; STIC-Biotech/ChemLib RE: In Re:10/054354 Sequence Search

Please rush. Thanks Chris

Chris Chan TC 1600 New Hire Training Coordinator and SPE 1644 308-3973 CM-1, 9B19

----Original Message-----

From:

Ford, Vanessa

Sent:

Wednesday, September 03, 2003 9:21 PM

T:

Chan, Christina

Subject:

In Re:10/054354 Sequence Search

Please search SEQ ID NO: 1

Please include interference searches. Please rush.

Vanessa L. Ford Biotechnology Patent Examiner

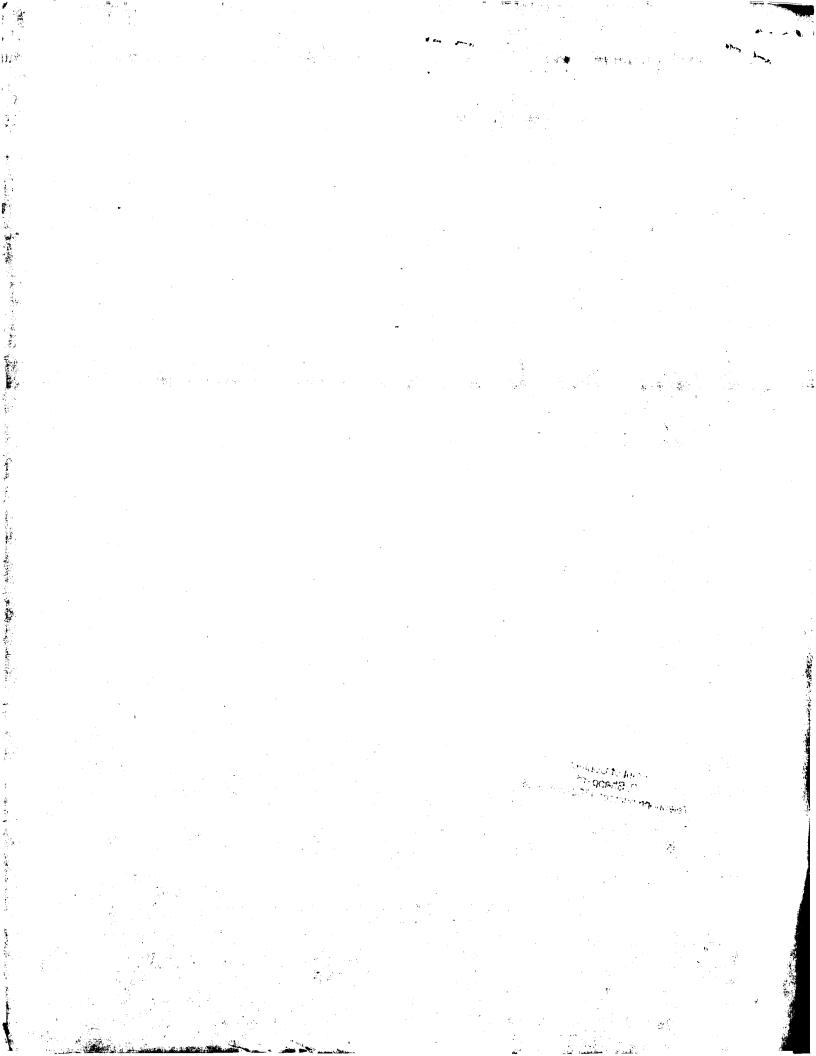
Office: CM1 8D17 Mailbox: CM1 8E12 Phone: 703.308.4735

> Point of Contact Telephone number: (703) 308-4499

Searcher:
Phone:
Location:
Date Picked Up:
Date Completed: 9/7/03
Searcher Prep/Review:
Clerical:
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TYPE OF SEARCH:
NA Sequences:
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Anaplasmataceae; Ebrlichia.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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MEDLINE=99242757; PubMed=10225842;
MCBTAINE=99242757; PubMed=10225842;
MCBTAIde J W. Yu, Xi, Xi Walker D.H.;
MOJecular cloning of the gene for a conserved major immunoreactive
28-kilodalton protein of Ehrlichia canis: a potential serodiagnostic
antigen."
Clin. Diagn. Lab. Immunol. 6:392-399 (1999).
EMBL; AF082748; AAC64554.1; -
InterPro; IFR002566; Surface Ag_msp4.
Pfem; PF01617; Surface Ag_2; 1.
NON_TER 278 278
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Anaplasmataceae; Ehrlichia.
NCBI_TaxID=944;
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Anaplasmataceae, Ehrlichia.
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28 kDa outer membrane protein (Fragment).
Ehrlichia canis.
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Matches 20; Conservative 0; Mismatches 0;
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EMBL; AF082750; AAC64556.1; -.

Interpro; IPR002566; Surface_Ag_msp4.

Pfam; PF01617; Surface_Ag_2; 1.

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MEDLINE=9924757; PubMed=10225842;
MEDLINE=9924757; PubMed=10225842;
MCBride J.W., Yu. Xj, Walker D.H.;
"Molecular cloning of the gene for a conserved major immunoreactive
"Molecular cloning of the gene for a conserved major immunoreactive
28-kilodalton protein of Ehrlichia canis: a potential serodiagnostic
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28 kDa outer membrane protein (Fragment).
Ehrlichia canis.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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100.0%; Pred. No. 2.8e-09;
ative 0; Mismatches 0;
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EMBL; AF082747; AAC64553.1; -.
InterPro; IPR002566; Surface_Ag_msp4.
NOM_TER 278 278 278-2; 1.
                                                                                                                                                         278 AA
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EMBL; AF082746; AAC64552.1; -.
InterPro; IPR002566; Surface_Ag_msp4.
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NON_TER 278 278
        KSTVGVFGLKHDWDGSPILK
                                              60 KSTVGVFGLKHDWDGSPILK
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J. Clin. Microbiol. 36:2671-2680(1998)
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Matches 20; Conservative
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SEQUENCE FROM N.A.
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01-MAY-1999
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
28 kDa outer membrane protein (Fragment).
Ehrlichia canis.
Bacteria, Proteobacteria, Alphaproteobacteria; Rickettsiales;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
28 kDa outer membrane protein (Fragment).
Ehrlichia canis.
Bacteria; Proteobacteria, Alphaproteobacteria; Rickettsiales;
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Pred. No. 2.8e-09;
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EMBL, AF082745; AAC64551.1; -.
Interpro; IPR002566; Surface Ag msp4.
Pfam, PF01617; Surface Ag_2; 1.
NON TER 278 278 278
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Clin. Diagn. Lab. Immunol. 6:392-399(1999).
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InterPro; IPR002566; Surface_Ag_msp4.
Pfam; PF01617; Surface_Ag_2; 1.
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60 KSTVGVFGLKHDWDGSPILK
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                                                                                                                                                                                                                                                                       Anaplasmataceae, Ehrlichia.
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Anaplasmataceae; Ehrlichia.
                                                                                                                                                                                                                Ehrlichia canis.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIJNE=98371112; PubMed=9705412;
Ohashi N., Unver A., Zhi N., Rikihisa Y.;
"Cloning and characterization of multigenes encoding the
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Interpro; IPR002566; Surface Ag msp4.
Pfam; PF01617; Surface Ag 2; 1.
SEQUENCE 307 AA; 34108 MW; 9DA9FD63EBF8BC97 CRC64;
                                                                                         01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Major outer membrane protein P30-1.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
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307
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                                                           Created)
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MEDLINE=21153566; PubMed=11254561;
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PRT;
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STRAIN=St.Vincent;
MEDLINE=99175287; PubMed=10074538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Arkansas;
MEDLINE=98321180; Pubmed=9647746;
                                                                                                                                                                                                                                                                                                                                                                                                                chaffeensis.";
Infect. Immun. 69:2083-2091(2001)
                                                                                                                                                     STRAIN-Arkansas;
MEDLINE-98084465; Pubmed-9423849;
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SEQUENCE 280 AA; 30731 MW;
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Best Local Similarity 73.7
Matches 14; Conservative
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                    OMP-1F.
Ehrlichia chaffeensis.
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                                                                                                                                  SEQUENCE FROM N.A.
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Major outer membrane protein OMP-1F (28kDa outer membrane protein gene
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McBride J.W., Yu, Xj, Walker D.H.; "Molecular cloning of the gene for a conserved major immunoreactive 28-kilodalton protein of Ehrlichia canis: a potential serodiagnostic
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                                                           Major Outer
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McBride J.W., Yu X.J., Walker D.H.;
"A conserved, transcriptionally active p28 multigene locus of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Anaplasmataceae, Ehrlichia.
                                                                                                                                                                                                                                    2; Length 280;
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                                                                                                                                                                                                                    71.8%; Score 79; DB 2; Length 280
82.4%; Pred. No. 0.00023;
V. maitches 2; Indels
                                                                             Membrane Protein Multigene Family in Ehrlichia canis and
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                                                                                                                                  EMBL; AR078553; AAK28699.1; -.
InterPro; IPR002566; Sufface Ag msp4.
Pfam; PF01617; Surface Ag 2: 1.
SEQUENCE 280 AA; 30803 MW; 27238BEIC7E68A91 CRC64;
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InterPro; IPR002566; Surface Ag msp4.
Pfam; PF01617; Surface Ag 2; 1.
SEQUENCE 280 AA; 30762 MW; BE284A4B94FE3123 CRC64;
                                                           Gene Clusters
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Last sequence update)
Last annotation update)
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                                      Ohashi N., Rikihisa Y., Unver A.;
"Analysis of Transcriptionally Active
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(TrEMBLrel. 06, Last seq
(TrEMBLrel. 23, Last anno
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                  MEDLINE=21153566; PubMed=11254561;
                                                                                             chaffeensis.";
Infect. Immun. 69:2083-2091(2001).
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                                                                                                                                                                                                                                                                                                                                           STVGVFGLKHDWNGGTI 76
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82.4%;
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Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                                                                                                                                           14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Gene 254:245-252(2000)
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01-JUN-1998
01-MAR-2003
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PubMed=12496165;
Cheng C., Paddock C.D., Ganta R.R.;
Cheng C., Paddock C.D., Ganta R.R.;
"Molecular Heterogeneity of Ehrlichia chaffeensis Isolates Determined
by Sequence Analysis of the 28-Kilodalton Outer Membrane Protein Genes
and Other Regions of the Genome.";
Infect. Immun. 71:187-195 (2003).
                                                                                                                                                                                                                                      Ohashi N., Zhi N., Zhang Y., Rikihisa Y.; Immunodominan major outer membrane proteins of Bhrlichia chaffeensis are encoded by a polymorphic multigene family."; Infect. Immun. 66:132-137(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21153356; PubMed=11254561;
Manshi N., Rikihisa Y., Unver A.;
"Analysis of Transcriptional Active Gene Clusters of Major Outer
Membrane Protein Multigene Family in Ehrlichia canis and E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reddy G.R., Sulsona C.R., Barbet A.F., Mahan S.M., Burridge M.J.,
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01-MAR-2003 (Tremblrel. 13, Last sequence update)
01-MAR-2003 (Tremblrel. 23, Last annotation update)
Outer membrane protein p28 (Fragment).
Ehrlichia chaffeensis.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Anaplasmataceae; Ehrlichia.
NCBI_TaxID=945;
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Ehrlichia.
NCBI_TaxID=945;
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73.7%; Pred. No. 0.00069;
iive 1; Mismatches 4; Indels
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; CCAA6C34E2AF393E CRC64;
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EMBL; AF479834; AA012937.1;
InterPro; IPR002566; Surface Ag_msp4.
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Length 276;

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Cheng C., Paddock C.D., Ganta R.R.;
"Molecular Heterogeneity of Ehrlichia chaffeensis Isolates Determined
by Sequence Analysis of the 28-Kilodalton Outer Membrane Protein Genes
and Other Regions of the Genome.";
Infect. Immun. 71:187-195(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    outer membrane protein gene
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Long S.W., Zhang X.-F., Qi H., Standaert S., Walker D.H., Yu X.-J
"Allele variation and patterns of transcription of the Ehrlichia
chaffeensis 28 kDa outer membrane protein multigene family.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                           ol-worlyy8 (TrEMBLrel, 08, Last sequence update)
01-MAR-2003 (TrEMBLrel, 23, Last annotation update)
Outer membrane protein p28 (28 kDa outer membrane protein).
Ehrlichia chaffeensis.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
MOBI TavTh-04
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
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Pfam; PF01617; Surface Ag 2; 1.
SEQUENCE 276 AA; 30027 MW; 2FD3698FCFIF60BE CRC64;
    Pfam; PF01617; Surface Ag_2; 1.
SEQUENCE 276 AA; 30028 MW; 2D7143AFCBFF2EBE CRC64;
                                                                       Query Match 66.4%; Score 73; DB 2; Best Local Similarity 76.5%; Pred. No. 0.002; Matches 13; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                   276 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yu X.J., McBride J.W., Walker D.H.; "Genetic diversity of the 28-kilodalton out human isolates of Bhrlichia chaffeensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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MEDLINE=99175287; PubMed=10074538;
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EMBL; AF077734; AAC31547.1; -.
EMBL; AY117397; AAL12925.1; -.
EMBL; AY117397; AAM7032.1; -.
EMBL; AF479835; AAO12943.1; -.
EMBL; AF479836; AAO12943.1; -.
                                                                                                                                                                     2 STVGVFGLKHDWDGSPI 18
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76.5%;
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Yu X.J., McBride J.W., Walker D.H.; "Genetic diversity of the 28-kilodalton outer membrane protein gene human isolates of Ehrlichia chaffeensis.";
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Long S.W., Zhang X.-F., Qi H., Standaert S., Walker D.H., Yu X.-J.;
"Allele variation and patterns of transcription of the Ehrlichia
chaffeensis 28 kDa outer membrane protein multigene family.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF393393, AAL12923.1;
InterPro; IPR002566; Surface_Ag_msp4.
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Anaplasmataceae; Ehrlichia.
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Anaplasmataceae; Ehrlichia.
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Pred. No. 0.0018; 3; Indels
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                                                                J. Clin. Microbiol. 37:1137-1143(1999).

EMBL; AF07735; AAC31548.1; -.

InterPro; IPR002566; Surface Ag_msp4.

Pfan; PF01617; Surface Ag_2; 1.

NON_TER 1

SEQUENCE 246 AA; 26884 MW; C9776392C5129A2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AF393389; AALI2919.1; -.
InterPro; IPR002566; Surface Ag_msp4.
Pfam; PF01617; Surface Ag_2; 1.
SEQUENCE 275 AA; 29974 MW; 2ECCF2F988B2E9D9 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 AA.
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Best Local Similarity 76.5%,
-hes 13; Conservative
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Best Local Similarity
Matches 13; Conserv
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Ehrlichia chaffeen
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                                                                                                                                                                                                                                                                                                                                                                            Variable surface a
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                                                                 AAU96110
ABG30749
ABG30745
AAY06942
          ABG77953
AAU96102
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16-JAN-2002; 2002WO-US01395
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O'Connor TP,
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Ehrlichia canis.
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RESULT 1
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Ehrlichia canis pe
Ehrlichia canis im
Ehrlichia canis p2
E. canis P30-1 pro
Ehrlichia canis ou
Ehrlichia chaffeen
E. canis P30-2 pro
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Ehrlichia chaffeen
                                                                            4 ; Search time 82 Seconds
(without alignments)
38.714 Million cell updates/sec
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The patent relates to homologous 28-kiloDalton (kDa) protein genes of Ehrlichia canis, designated ECa28SA1, ECa28SA2, ECa28SA3, ECa28SA3, ECa28SA2, ECa28SA3, ECa28SA2, ECa28SA3, ECa28-1 and ECa28-2. These genes are members of a polymorphic multiple gene family and contained in a single locus of 5.59 kb. The 28-kDa proteins are immunoreactive with anti-E. canis serum hence are important immunoprotective antigens. The protein is useful for vaccinating against E. canis infections such as canine ehrlichiosis in dogs. Canine ehrlichiosis, also known as canine tropical pancytopaenia, is a tick-tick-tick-tick-to-farial disease of dogs. ECa28-1 is conserved amongst different strains of E. canis and hence useful for serodiagnosis of canine ehrlichiosis. The present sequence is a E. canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECa28-1 30-kDa protein which is post-translationally modified to mature 28-kDa protein by cleavage of N-terminal signal sequence.
                                                                                                                                                                                                                                                                                                                                                                               Ehrlichia canis antigens useful for vaccinating against canine ehrlichiosis in dogs -
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                                                                                                                                                                                                                      Walker DH, Yu X, McBride JW;
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99WO-US28075
                                                              98US-0201458
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                                                                                                                                                           (RERE-) RES DEV FOUND.
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                                                           30-NOV-1998;
   24-NOV-1999;
                                                                                            03-MAR-1999;
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                                                                                     The invention relates to a composition of matter comprising a polypeptide isolated from Enrichia species. The composition can be used for detecting the presence of antibodies to Enrichia, comprising contacting one or more polypeptides with a test sample suspected of comprising antibodies to Ehrlichia, under conditions that allow polypeptide/antibody complexes to form and detecting the complexes, where the detection of polypeptide/antibody complexes is an indication that antibodies to Ehrlichia are present in the test sample. The composition is useful for detection in mammals. The polypeptides can be used to develop monoclonal and/or polyclonal antibodies that can be employed in assay systems and in the generation of chimeric antibodies for therapeutic use or other similar applications. This sequence represents an E. canis peptide fragment used in the composition of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homologous 28-KDa protein gene; ECa28-1; immunoreactive; vaccine; p28 gene; p01vmorphic multiple gene family; immunoprotective antigen; antibacterial; canine ehrlichiosis; canine tropical pancytopaenia; tick-borne ricketteial disease; serodiagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 20;
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cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /6..84
//abel= Variable_region_2
//note= "contains immunoreactive peptides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246.258
/label= Variable region 4
/note= "contains immunoreactive peptides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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/label= Variable_region_1
/note= "contains immunoreactive peptides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48..156
|abel= Variable_region_3
note= "contains immunoreactive peptides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1..23
label= Signal_peptidase_cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.278
label= Mature_ECa28-1_28-kDa_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 110; DB 23;
100.0%; Pred. No. 2.5e-11;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ehrlichia canis immunoreactive protein ECa28-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..23
label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY71477 standard; Protein; 278 AA.
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                                    Claim 1; Page 5; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ehrlichia canis.
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Query Match

Matches

ઠે a RESULT 2

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Gaps

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Length 278; Indels New recombinant homologous 28 kilodalton immunodominant protein from

08-JUN-2000

Protein Peptide

Region

Region

Region

Region

Sequence

Query Match Best Local

Matches

AAY06961;

RESULT 4 AAY06961

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The invention relates to an isolated polynucleotide encoding an outer membrane protein (OMP) of Ehrlichia canis or Ehrlichia chaffeensis used in the diagnosis of infection. An infection such as human ehrlichiosis or canine ehrlichiosis can be diagnosed by providing a serum sample from the patient, providing a polypeptide or mixture of polypeptides, contacting the sample with the polypeptide and assaying for the formation of a complex between antibodies in the semum sample and the polypeptide, where formation of a complex is indicative of infection with E. chaffeensis. This sequence represents an Ehrlichia outer membrane protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated polynucleotide encoding an Outer membrane protein of E.canis or E.chaffeensis used in the diagnosis of infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAP1 homologue; variable surface antigen; VSA4; rickettsia;
DNA vaccine.
                                                                                                                                                                                                                                                           Outer membrane protein; OMP; P30F; ehrlichiosis; infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match .100.0%; Score 110; DB 23;
Best Local Similarity 100.0%; Pred. No. 5.9e-10;
                                                                                                                                                                                                                    Ehrlichia canis outer membrane protein (P30F) #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                  ABG77952 standard; Protein; 307 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW51094 standard; Protein; 280 AA
      89 KSTVGVFGLKHDWDGSPILK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kstveveckhowbespirk 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 10; Fig 21B; 49pp; English
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                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-618954/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (RIKI/) RIKIHISA Y. (OHAS/) OHASHI N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABS63293
                                                                                                                                                                                                                                                                                             Ehrlichia canis.
                                                                                                                                                                                                                                                                                                                                     US2002120115-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-MAY-1999;
                                                                                                                                                                              15-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                           29-AUG-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention
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                                                                                                                                          ABG77952;
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                                                                RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in AAY06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAY06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                          The invention relates to a recombinant homologous 28 kDa immunodominant protein, P28, (I), of Ehrlichia canis. (I), a 28-kDa antigen preferably dispersed in a pharmaceutically acceptable carrier, is useful for inhibiting E. canis infection in a subject. (I) is useful in the development of vaccines and serodiagnostics that are particularly effective for disease prevention and serodiagnosis. AAU95100-AAU95118 represent the 28-kDa antigen amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
Ehrlichia canis, useful for treating Ehrlichia canis infections
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                                                                                                                                                                                                                                                                           Length 278;
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                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                         100.0%; Score 110; DB 23;
100.0%; Pred. No. 5.3e-10;
ive 0; Mismatches 0;
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100.0%; Pred. No. 5.9e-10;
ive 0; Mismatches 0;
                                      Claim 16; Figure 1; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Fig 21B; 55pp; English
                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                           60 KSTVGVFGLKHDWDGSPILK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KSTVGVFGLKHDWDGSPILK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY06961 standard; Protein; 307
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                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E. canis P30-1 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-254290/21.
N-PSDB; AAX34761.
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                   278 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             307 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ehrlichia canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection; dog
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Gaps

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Indels

Length 307;

Location/Qualifiers

Ehrlichia chaffeensis,

97WO-US19044. 96US-0733230

17-OCT-1997; 17-OCT-1996;

23-APR-1998

WO9816554-A1

Peptide

Barbet AF, Burridge MJ, Nyika A, Rurangirwa FR;

WPI; 1998-251232/22.

N-PSDB; AAV07179.

(UYFL) UNIV FLORIDA

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The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1. -1(B to Z) shown in AAY06941-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAY06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides useful as DNA vaccines for conferring immunity to rickettsial infection e.g. heartwater caused by Cowdria ruminantium, comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ganta RR, Burridge MJ, Mahan SM, McGuire TC;
Id AL, Simbi BH, Whitmire WW, Alleman AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ehrlichia chaffeensis; VSA4; variable surface antigen 4; MAP1; major antigenic protein 1; antirickettsia1; vaccine; gene therapy; Rickettsia; Cowdria; Anaplasma; map2; lhworf3; 4hworf1; 18hworf1;
                                                                                                                                                                                                               Novel outer membrane proteins from Ehrlichia chaffeensis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.8%; Score 79; DB 20; Length 280; 82.4%; Pred. No. 7.8e-05; Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ehrlichia chaffeensis partial VSA4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB36188 standard; Protein; 280 AA.
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                                                                                                                                                                                                                                                                        Disclosure; Fig 22B; 55pp; English
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FR, Moreland AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-APR-2000; 2000WO-US10886.
98WO-US19600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-APR-1999; 99US-0130725
                                      97US-0059353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STVGVFGLKHDWNGGTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 STVGVFGLKHDWDGSPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                           (OHIS ) UNIV OHIO STATE.
                                                                                                               Rikihisa Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ehrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-679675/66.
N-PSDB; AAC68705.
                                                                                                                                                        WPI; 1999-254290/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 AA;
                                                                                                                                                                          N-PSDB; AAX34762
                                                                                                                                                                                                                                     Ehrlichia canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rurangirwa FR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200065063-A2.
18-SEP-1998;
                                      19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barbet AF,
                                                                                                                 Ohashi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB36188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the full-length variable surface antigen VSA4 protein of Ehrlichia chaffeensis. Its amino acid sequence was deduced from a partial open reading frame (ORF4) of a genomic locus (see AAV07179) of E. chaffeensis that was obtained on the basis of homology to the major antigenic protein MAP1 (see AAW51088) of Cowdria ruminantium. This genomic locus included S ORFs encoding similar, but comprises a nucleic acid (see AAV871081-95). A claimed composition comprises a nucleic acid (see AAV07176-82) encoding a polypeptide (see AAW51088-99) that ellicits a protective immune response against crickettsial pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Rickettsia, Ehrlichia, Anaplasma and Cowdria species. The Ehrlichia antigenic associated with Ehrlichia infection (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition containing nucleic acid encoding rickettsial antigen - useful for, e.g. stimulating protective immune response in humans or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                 Ganta RR, Mahan SM, McGuire TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 79; DB 19; Length 20.
Pred. No. 7.8e-05;
                                                          1..25
/note= "putative signal peptide"
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AAY06962 standard; Protein; 280 AA

RESULT 7 AAY06962 E. canis P30-2 protein.

05-JUL-1999

AAY06962;

Ehrlichia canis. detection; dog

X B X B X S X K K X B X B X Y X X

WO9913720-A1

25-MAR-1999

20

2 STVGVFGLKHDWDGSPILK

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71.8%; 73.7%;

Local Similarity 73.7 res 14; Conservative

Matches

280 AA;

Sequence Query Match ö

Gaps

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Claim 3; Fig 2B; 39pp; English.

animals

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Sequence
                                                                                                                                    Query Match
                                                                                                                                                                                                                                       RESULT 10
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ID AAUC
 88888888888888
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        The present sequence shows a high degree of similarity to the major antigenic protein 1 (MAP1) of Ehrlichia sp. The MAP1 gene may be used in a vaccines to protect animals or humans against rickettsial diseases caused by a organisms of Rickettsia sp., Ehrlichia sp., Anaplasma sp. or Cowdria sp. The vaccine elicits an immune response protective against the rickettsial pathogen. The nucleic acid vaccines can be driven by the human cytomegalovirus (HCMV) enhancer-promoter. Cowdria ruminatium genes designated map 2, Ihworf3, 4hworf1, 18hworf1 and 3dorf3 may be used in therapeutic and diagnostic applications. The polypeptides are useful for detecting antibodies associated with infection by a rickettsial pathogen whilst the polymucleotides may be used to detect the presence of rickettsial nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The patent relates to homologous 28-kiloDalton (kDa) protein genes of Bhrllchia canis, designated BCa288A1, BCa288A2, BCa288A3, BCa288-1 and BCa38-2. These genes are members of a polymorphic multiple gene family and contained in a single locus of 5.592 kb. The 28-kDa proteins are
                                                                                                                                                                                                                                                                                                                                                                                             Homologous 28-kDa protein gene; BCa28SA3; immunoreactive; vaccine; p28 gene; polymorphic multiple gene family; immunoprotective antigen; antibacterial; canine ehrlichiosis; canine tropical pancytopaenia; tick-borne rickettsial disease; serodiagnosis.
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ehrlichia canis antigens useful for vaccinating against canine ehrlichiosis in dogs -
                                                                                                                                                                               Score 79; DB 21; Length 280;
Pred. No. 7.8e-05;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24..280
/label= Mature_ECa28SA3_28-kDa_protein
                                                                                                                                                                                                                                                                                                                                                                         Ehrlichia canis immunoreactive protein ECa28SA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1..23
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Page 68-69; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                        AAY71479 standard; Protein; 280 AA.
                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                        2 STVGVFGLKHDWDGSPILK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yu X, McBride JW;
                                                                                                                                                                             Query Match
Best Local Similarity 73.7%;
Matches 14; Conservative 2
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99US-0261358.
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N-PSDB; AAD01294, AAD01295.
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                                                                                                                                                         280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ehrlichia canis.
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                                                                                                                                                                                                                                                                                                                             AAY71479;
                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                  RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New MAP2 genes and polypeptides useful as vaccines for conferring immunity to human and animal rickettsial diseases, e.g. heartwater, or as molecular markers in nucleic acid analysis procedures
immunoreactive with anti-E. canis serum hence are important immunoprotective antigans. The protein is useful for vaccinating against E. canis infections such as canine ehrlichiosis in dogs. Canine ehrlichiosis, also known as canine tropical pancytopaenia, is tick-borne rickettsial disease of dogs. ECa28-1 is conserved amongst different strains of E. canis and hence useful for serodiagnosis of canine ehrlichiosis. The present sequence is a E. canis ECa2853 30 kDa protein which is post-translationally modified to a mature 28-kDa protein by cleavage of N-terminal signal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Major antigenic protein; MAP; vaccine; immunogenic; rickettsia; infection; heartwater; diagnostic; variable surface antigen; VSA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Variable surface antigen 4 (VSA4) from Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.8%; Score 79; DB 21; Length 280; 82.4%; Pred. No. 7.8e-05; ive 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barbet AF, Ganta RR, McGuire TC, Burridge MJ, Rurangirwa FR, Mahan SM, Bowie MV, Alleman AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Fig 2A-2B; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU04198 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 STVGVFGLKHDWDGSPI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STVGVFGLKHDWNGGTI 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYFL ) UNIV FLORIDA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 14; Conserv
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Sequence

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Query Match

Matches

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The invention relates to a recombinant homologous 28 kDa immunodominant protein, P28, (I), of Ehrlichia canis. (I), a 28 kDa antigen preferably dispersed an antigen preferably dispersed in a pharmaceutically acceptable carrier, is useful for inhibiting E. canis infection in a subject. (I) is useful in the development of vaccines and serodiagnostics that are particularly effective for disease prevention and serodiagnosis. AAUS6100-AAUS6118 represent the 28-kDa antigen amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant homologous 28 kilodalton immunodominant protein from Ehrlichia canis, useful for treating Ehrlichia canis infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ehrlichia; outer membrane protein; P28; antibiotic; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.8%; Score 79; DB 23; Length 280; 82.4%; Pred. No. 7.8e-05; ive 1; Mismatches 2; Indels
                                                                                Ehrlichia canis infection; vaccine; serodiagnostic; p28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ehrlichia chaffeensis outer membrane protein P28-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU73417 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 16; Figure 7; 106pp; English
                                                                                                                                                                                                                                                                                                                                     Yu X, McBride JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 STVGVFGLKHDWDGSPI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000; 2000US-201035P.
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               02-JUL-2002 (first entry)
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                                             Ehrlichia canis p28-6.
                                                                                                                                                                                                                                                                                                      (RERE-) RES DEV FOUND
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-351882/38.
N-PSDB; ABK68854.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 AA;
                                                                                                                                 Ehrlichia canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200183699-A2.
                                                                                                                                                                  WO200222782-A2
                                                                                                   antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAR-2002
                                                                                                                                                                                                    21-MAR-2002.
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                                                                                                                                                                                                                                                                                                                                       Walker DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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Best Local {
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AAU73417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated polynucleotide encoding an outer membrane protein (OMP) of Ehrlichia canis or Ehrlichia chaffeensis used in the diagnosis of infection. An infection such as human ehrlichiosis or canine ehrlichiosis can be diagnosed by providing a serum sample from the patient, providing a polypeptide or mixture of polypeptides, contacting complex between antibodies in the serum sample and the polypeptide with the serum sample and the polypeptide, where formation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated polynucleotide encoding an outer membrane protein of E.canis or E.chaffeensis used in the diagnosis of infection -
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence represents an Ehrlichia outer membrane protein of
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                               Score 79; DB 22; Length 280;
Pred. No. 7.8e-05;
2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                       Outer membrane protein; OMP; P30F; ehrlichiosis; infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 79; DB 23; Le
Pred. No. 7.8e-05;
                                                                                                                                                                                                                                                                                                                       Ehrlichia canis outer membrane protein (P30F) #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU96102 standard; Protein; 280 AA.
                                                                                                                                                                                                                     ABG77953 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 10; Fig 22B; 49pp; English
                                                                                                   2 STVGVFGLKHDWDGSPILK 20
                                                                                                                       5;
                                 71.8%;
73.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JAN-2002; 2002US-0059964,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0314701
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                                                                                                                                                                                                                                                                                      (first entry)
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                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-618954/66.
N-PSDB; ABS63294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (RIKI/) RIKIHISA Y.
                                               Local Similarity
nes 14; Conserv
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Les 14; Conserv
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280 AA;
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                                                                                                                                                                                                                                                                                                                                                                                      Ehrlichia canis.
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19-MAY-1999;

Sequence

This

Query Match

Matches

ò a a AAU96102;

SX5

RESULT 12 AAU96102

29-AUG-2002.

15-NOV-2002

ABG77953;

RESULT 11

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Gaps

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Gaps

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The invention relates to an isolated polynucleotide encoding an outer membrane protein (OMP) of Ehrlichia canis or Ehrlichia chaffeensis used in the diagnosis of infection. An infection such as human ehrlichiosis or canine ehrlichiosis can be diagnosed by providing a serum sample from the patient, providing a polypeptide or mixture of polypeptides, contacting the sample with the polypeptide and assaying for the formation of a complex between antibodies in the serum sample and the polypeptide, where formation of a complex is indicative of infection with E. chaffeensis. This sequence represents an Ehrlichia outer membrane protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated polynucleotide encoding an outer membrane protein of E.canis or E.chaffeensis used in the diagnosis of infection -
                                                                                                                                                                                                                                               Outer membrane protein; OMP; P30F; ehrlichiosis; infection.
                                                                                                                                                                                                                   Ehrlichia chaffeensis outer membrane protein (OMP)
    Mismatches
                                                                                                                              ABG77940 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 8B; 49pp; English.
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                                2 STVGVFGLKHDWDGSPILK
                                               STVGVFGLKHDWDGSPILK
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73.7%;
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                                                                                                                                                                                                                                                                                                                                                                                           99US-0314701
                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 69.1
Best Local Similarity 73.7
Matches 14; Conservative
    14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: September
Job time: 83 secs
                                                                                                                                                                                                                                                                          Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rikihisa Y, Ohashi N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-618954/66.
                                                                                                                                                                                                                                                                                                                                                                                                                      (RIKI/) RIKIHISA Y.
(OHAS/) OHASHI N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 AA;
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                                                                                                                                                            ABG77940;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1. -1(B to Z) shown in AAV06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAV06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                        P28
                                                       Novel Ehrlichia chaffeensis 28-kDa outer membrane protein, designated
P28 useful as a vaccine against Ehrlichia chaffeensis
                                                                                                                           The invention relates to isolated and purified 28-kDa outer membrane proteins (P28-1 to P28-21) of Ehrlichia chaffeensis. P28 proteins are encoded by a 28kDa outer membrane protein multigene family. P28 proteins are useful as a vaccine against E.chaffeensis. DNA encoding is useful for transfecting a host cell, AAU73400-AAU73420 represent Ehrlichia chaffeensis P28 outer membrane proteins of the invention.
                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          outer membrane proteins from Ehrlichia chaffeensis and
                                                                                                                                                                                                                                                          DB 23; Length 280; 7.8e-05; ches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 76; DB 20; Length 280;
Pred. No. 0.00025;
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                                                                                                                                                                                                                                                           Score 79;
Pred. No.
                                                                                                Disclosure; Figure 2; 97pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                   AAY06948 standard; Protein; 280 AA.
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73.7%;
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Best Local Similarity 73.7%;
Matches 14; Conservative
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N-PSDB; AAX34748.
                             WPI; 2002-066527/09
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Best Local Similarity
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 Yu X;
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Score 76; DB 23; Length 280;
Pred. No. 0.00025;
1; Mismatches 4; Indels
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Scoring table:

Searched:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

OM protein

Run on:

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Sequence 2, Application US/09261358A

Patent No. 6403780

GENERAL INFORMATION:
APPLICANT: Walker, David H.
APPLICANT: Walker, David H.
APPLICANT: Walker, David H.
TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
TITLE REFERENCE: D6152CIP
CURRENT APPLICATION NUMBER: US/09/261,388A
CURRENT FILING DATE: 1999-03-03
PRIOR APPLICATION NUMBER: 09/201,458
PRIOR APPLICATION NUMBER: 09/201,458
PRIOR FILING DATE: 1998-11-30

NUMBER OF SEQ ID NOS: 33
SEQ ID NO 2
                                                     Sequence
Sequence
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; OTHER INFORMATION: amino acid sequence of E. canis p28-7 protein
[02-09-660-587-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 110; DB 4; Length 278; 100.0%; Pred. No. 7e-11; ive 0; Mismatches 0; Indels
             US-09-201-458-8
US-09-314-701-8
US-09-314-701-42
US-09-60-587-44
US-09-60-587-13
US-09-261-358A-13
US-09-201-458-9
US-09-201-458-7
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Best Local Similarity 100.0
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ORGANISM: Ehrlichia canis
RESULT 2
US-09-261-358A-2
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LENGTH: 278
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                                                                                                                          5, 2003, 14:05:34; Search time 28 Seconds (without alignments) 30.222 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36, Sequence 17, Sequence 6, A Sequence 14, Sequence 14, Sequence 11, Sequence 12, Sequence 18, Sequence 4, A Sequence 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15,
Sequence 15,
Sequence 11,
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Sequence 2, A
Sequence 2, A
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Sequence 9, 1
Sequence 5, 1
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/cgn2 6/ptcdata/1/iaa/5B_COMB.pep:*
/cgn2 6/ptcdata/1/iaa/6A_COMB.pep:*
/cgn2 6/ptcdata/1/iaa/6B_COMB.pep:*
/cgn2 6/ptcdata/1/iaa/PCTUS COMB.pep:*
/cgn2 6/ptcdata/1/iaa/PCTUS COMB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-261-356A-2

US-09-201-368-2

US-09-314-701-36

US-09-561-356A-6

US-09-261-356A-14

US-09-261-356A-14

US-09-261-356A-14

US-09-201-458-10

US-09-201-458-10

US-09-201-458-10

US-09-201-458-10

US-09-313-230-4

US-09-313-230-4

US-09-313-230-4

US-09-314-701-2

US-09-314-701-2

US-09-314-701-2

US-09-314-701-32

US-09-313-326-15
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                                                                                                                                                                                                                                                                                                                                      328717 seqs, 42310858 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                        - protein search, using sw model
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1 KSTVGVFGLKHDWDGSPILK 20
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seq length: 200000000
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Match Length
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Score

Result No.

11110 11110 11110 11100 1100 10

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Gaps

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TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: Animals and Humans FILE REPERENCE: UP-1670.

FULE REPERENCE: UP-1670.

CURRENT APPLICATION NUMBER: US/08/953,326

EARLIER APPLICATION NUMBER: 08/953,326

EARLIER FILING DATE: 1997-10-17

EARLIER APPLICATION NUMBER: 08/733,230

EARLIER FILING DATE: 1996-10-17

NUMBER: PECHING DATE: 1996-10-17

SOFTWARE: PECHIN Ver: 2.0

SOFTWARE: PECHIN Ver: 2.0
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Pred. No. 1.3e-05;
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Pred. No. 1.3e-05
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73.7%; Pred. No. 1:-
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                89 KSTVGVFGLKHDWDGSPILK 108
                                                                                                            Sequence 17, Application US/08953326
Patent No. 6251872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 STVGVFGLKHDWDGSPILK 20
                                                                                                                                                                  APPLICANT: Barbet, Anthony F. APPLICANT: Ganta, Roman R. APPLICANT: McGuire, Travis C. APPLICANT: Burridge, Michael J. APPLICANT: Nyika, Aceme APPLICANT: Rurangirwa, Fred R. APPLICANT: Mahan, Suman M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Ehrlichia chaffeensis
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61 TTIGVFGLKQDWDGSTISK
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82.4%;
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Best Local Similarity 82.4 Matches 14; Conservative
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ORGANISM: Ehrlichia canis
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                                                                                                                                                  GENERAL INFORMATION:
                                                                                              US-08-953-326-17
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US-09-660-587-6
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APPLICANT: Rikihisa, Yasuko
APPLICANT: Ohasi, No. 654517io
APPLICANT: Onasi, No. 654517io
TITLE OF INVENTION: Outer Membrane Protein of Ehrlichia and Ehrlichia
TITLE OF INVENTION: Chaffeensis
FILE REFERENCE: 22727/04021
CURRENT APPLICATION NUMBER: US/09/314,701
CURRENT FILING DATE: 1999-05-19
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: Walker, David H.

APPLICANT: McBride, Jere W.

APPLICANT: McBride, Jere W.

APPLICANT: Yu, Xue Vere W.

TITLE OF INVENTION: 28-kDa Immunoreactive Protein Gene of Ehrlichia TITLE OF INVENTION: canis and Uses Thereof FILE REFERENCE: D6152

CURRENT APPLICATION NUMBER: US/09/201,458A

CURRENT FILING DATE: 1998-11-30

NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: amino acid sequence of a 30 kDa immunoreactive OTHER INFORMATION: protein of Ehrlichia canis
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                                                                                                                                Score 110; DB 4; Length 278;
Pred. No. 7e-11;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 110; DB 4; Length 278; 100.0%; Pred. No. 7e-11; Aztive 0; Mismatches 0; Indels
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                                                          ; FEATURE:
; OTHER INFORMATION: amino acid sequence of ECa28-1 protein
US-09-261-358A-2
                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09201458A Patent No. 6458942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-314-701-36
; Sequence 36, Application US/09314701
; Patent No. 6544517
                                                                                                                                                                                                                1 KSTVGVFGLKHDWDGSPILK 20
                                                                                                                                                                                                                                    60 KSTVGVFGLKHDWDGSPILK 79
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                                                                                                                                    Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 20; Conservative 0
                  TYPE: PRT
ORGANISM: Ehrlichia canis
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TYPE: PRT
CRGANISM: Ehrlichia canis
US-09-314-701-36
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Best Local Similarity
Matches 20; Conserv
LENGTH: 278
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60 STVGVFGLKHDWNGGTI

1 KSTVGVFGLKHDWDGSPILK 20

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Genes of Ehrlichia canis and Uses Thereof
; TITLE OF INVENTION: Genes of Ehrlichia cani; FILE REFERENCE: D6152CIP2; CURRENT APPLICATION NUMBER: US/09/660,587; CURRENT FILING DATE: 2000-09-12; PRIOR PILING DATE: 1999-03-03; NUMBER OF SEQ ID NOS: 46; SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: D6152
CURRENT APPLICATION NUMBER: US/09/201,458A
CURRENT FILING DATE: 1998-11-30
NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-261-358A-14; Sequence 14, Application US/09261358A; Patent No. 6403780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TTTGVFGLKQDWDGSTISK 79
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                                                                                                                                                                                                                                    ORGANISM: Ehrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                                       Query Match 69.1%;
Best Local Similarity 73.7%;
Matches 14; Conservative
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Best Local Similarity 73.7<sup>3</sup>
Matches 14; Conservative
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US-09-201-458-10
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APPLICANT: Rikihisa, Yasuko
APPLICANT: Rikihisa, Yasuko
APPLICANT: Ohasi, No. 6544517io
APPLICANT: Ohasi, No. 6544517io
TITLE OF INVENTION: Outer Membrane Protein of Ehrlichia and Ehrlichia
TITLE OF INVENTION: Chaffeensis
FILE REFERENCE: 22727/04021
CURRENT APPLICATION NUMBER: US/09/314,701
CURRENT FILING DATE: 1999-05-19
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 38
LENGTH: 280
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                                                                                                                                GENERAL INCORNATION:
APPLICANT: Walker, David H.
APPLICANT: Walker, David H.
APPLICANT: Walker, Jere W.
APPLICANT: W. Xue-Jie
TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
FILE REPERENCE: D6152CIP
CURRENT APPLICATION NUMBER: US/09/261,358A
CURRENT FILING DATE: 1999-03-03
PRIOR APPLICATION NUMBER: 09/201,458
PRIOR PLICATION NUMBER: 09/201,458
RRIOR PLICATION NUMBER: 1999-11-30
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 66
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Patent No. 6392023
GENERAL INFORMATION:
APPLICANT: Walker, David H.
APPLICANT: McBride, Jere W.
APPLICANT: Yu, Xue-Jie
TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
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82.4%; Pred. No. 1.3e-05;
Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.8%; Score 79; DB 4; Length 280; 82.4%; Pred. No. 1.3e-05; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE: OTHER INFORMATION: amino acid sequence of ECa28SA3 protein
                                                                                          Sequence 6, Application US/09261358A
Patent No. 6403780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 38, Application US/09314701 Patent No. 6544517
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Best Local Similarity 82.4°
Matches 14; Conservative
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Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Ehrlichia canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Ehrlichia canis
US-09-314-701-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-261-358A-6
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US-09-314-701-38
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Gaps
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APPLICANT: Walker, David H.
APPLICANT: Walker, Jere W.
APPLICANT: Yu, Xue-Jie
APPLICANT: Yu, Xue-Jie
TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
FILE REFERENCE: D6152CIP
CURRENT APPLICATION NUMBER: US/09/261,358A
CURRENT FILING DATE: 1999-03-03
PRIOR APPLICATION NUMBER: 09/201,458
PRIOR APPLICATION NUMBER: 09/201,458
NUMBER OF SEQ ID NOS: 33
SEQ ID NO: 33
SEQ ID NO: 280
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Patent No. 6458942
GENERAL INFORMATION:
APPLICANT: Walker, David H.
APPLICANT: McBride, Jere W.
APPLICANT: VI, XUe - Jie
TITLE OF INVENTION: 28-4Da Immunoreactive Protein Gene of Ehrlichia
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; OTHER INFORMATION: amino acid sequence of E. chaffeensis OMP-1F
US-09-660-587-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: amino acid sequence of E. chaffeensis OMP-1F US-09-261-358A-14
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                                                                                                      Length 280;
                                                                                                Score 76; DB 4; 1 Pred. No. 4.2e-05;
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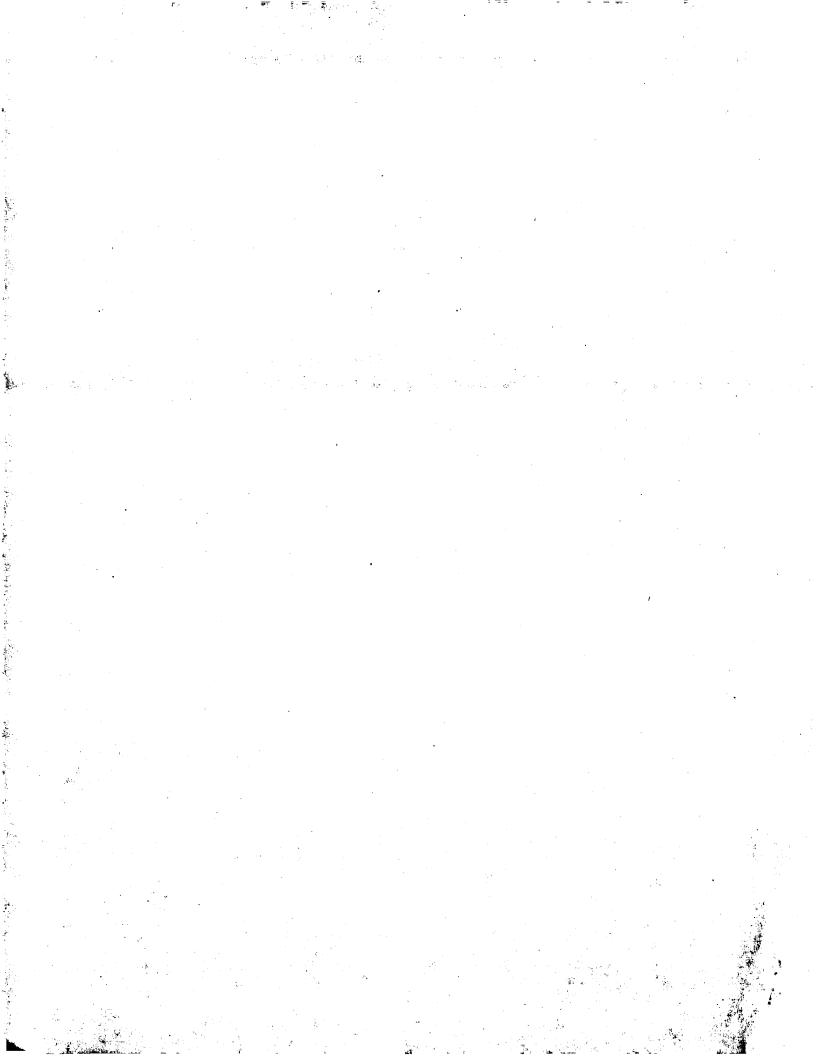
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Barbet
APPLICANT: Ganta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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JACENT NO. 62218/2/
JAPPLICANT: Barbet, Anthony F.
APPLICANT: Barbet, Anthony F.
APPLICANT: Bardia, Roman R.
APPLICANT: Burridge, Michael J.
APPLICANT: Burridge, Michael J.
APPLICANT: Nurangiraw, Fred R.
APPLICANT: Nurangiraw, Fred R.
APPLICANT: Nurangiraw, Fred R.
APPLICANT: Nurangiraw, Fred R.
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Animals and Humans
TITLE OF INVENTION: Animals and Humans
FILE REFERENCE: UF-167C1
CURRENT APPLICATION NUMBER: US/08/953,326
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER PILING DATE: 1997-10-17
EARLIER PILING DATE: 1997-10-17
EARLIER PILING DATE: 1996-10-17
NUMBER OF SEQ ID NOS: 24
NUMBER OF SEQ ID NOS: 24
NUMBER OF SEQ ID NOS: 24
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Patent No. 6544517

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rikihisa, Yasuko
APPLICANT: Chasi, No. 6544517io
TITLE OF INVENTION: Chaffeensis
FILE REPERENCE: 22727/04021
CURRENT APPLICATION NUMBER: US/09/314,701
CURRENT FILING DATE: 1999-05-19
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.0
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                                                                            , OTHER INFORMATION: amino acid sequence of E. chaffeensis OMP-1F US-09-201-458-10
                                                                                                                                        Query Match 69.1%; Score 76; DB 4; Length 280; Best Local Similarity 73.7%; Pred. No. 4.2e-05; Matches 14; Conservative 1; Mismatches 4; Indels
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Pred. No. 4.2e-05;
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                                                                                                                                                                                                                       2 STVGVFGLKHDWDGSPILK 20
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; ORGANISM: Ehrlichia chaffeensis
US-08-953-326-18
                    TYPE: PRT ORGANISM: Ehrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Ehrlichia chaffeensis US-09-314-701-12
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Best Local Similarity 73.7%;
Matches 14; Conservative
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LENGTH: 280
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                                                          FEATURE:
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                                                                                                                                                                                                                                                                                                                                                APPLICANT: McGuire, Travis C.
APPLICANT: Burridge, Michael J.
APPLICANT: Burridge, Michael J.
APPLICANT: Rurangirwa, Fred R.
APPLICANT: Rurangirwa, Fred R.
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against
TITLE OF INVENTION: Rickettsial Diseases and Methods of Use CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
SIRBET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 280;
65.5%; Score 72; DB 3; Length 276; 76.5%; Pred. No. 0.0002; cive .2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.5%; Score 72; DB 3; Length 280
76.5%; Pred. No. 0.0002;
tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSEE: Saliwanchik & Saliwanchik
F: 2421 N.W. 41st Street, Suite A-1
Gainesville
                                          2, Mismatches
                                                                                                                                                                                                                                                                                                       Barbet, Anthony F.
Ganta, Roman Reddy
McGuire, Travis C.
Burridge, Michael J.
                                                                                                                                                                                                                                          Sequence 4, Application US/08733230 Patent No. 6025338
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Patent No. 6251872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTATION UNDRER: 36,965
REFERENCE/DOCKET NUMBER: UF-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 STVGVFGLKHDWDGSPI 18
                                                                                     2 STVGVFGLKHDWDGSPI 18
                                                                                                                GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman R.
APPLICANT: McGuire, Travis C.
APPLICANT: Burridge, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 280 amino acids
amino acid
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Best Local Similarity 76.5.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-08-733-230-4
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28k surface antige major antigency program of a surface antige 28k surface antige 28k surface antige hypothetical prote 29k surface antige hypothetical prote tauropine dehydrog hypothetical prote hypothetical prote probable phosphogl dihydroxy-acid deh DNA-directed DNA probable NA directed DNA probable RTX famil
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                                                                                      %9 ; Search time 40 Seconds
(without alignments)
48.084 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                    283308 segs, 96168682 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                        5, 2003, 14:01:59
                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                          OM protein - protein search, using sw model
                                                                                                                                                               110
1 KSTVGVFGLKHDWDGSPILK 20
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Gapop 10.0 , Gapext 0.5
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JE0218
JE0219
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JE0221
AS9226
A97634
AC2857
AC2857
F75010
B89834
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S35137
G86777
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B87580
B85547
F90696
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Maximum DB seq length: 200000000
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                    PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                        September
                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                          Scoring table:
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                                                                                      Run on:
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No.
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sulfate transporte sulfate transporte hypotherical prote unknown protein, 5 hypotherical prote Cell division prot hypotherical prote hypotherical prote conserved hypother conserved hypother conserved hypother nADH2 dehydrogenas nadh oxidoredutas NADH2 dehydrogenas hypotherical prote branched-chain ami glycosyltransferas	ENTS	Ehrlichia chaffensis laffensis squence_revision 21-Aug-1998 #text_change 17-Mar-1999 C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, Commun. 247, 656-643, 1998 acterization of a 28kDa surface antigen gene family of the 1216; MUID:98321180; PMID:9647746	re 79; DB 2; Length 280; d. No. 6.3e-05; Mismatches 3; Indels 0; Gaps 0;	uaffensis on 21-Aug-1998 #text_change 17-Mar-1999 ., A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, 6.6 643, 1998 of a 28kDa surface antigen gene family of the 12180; PMID:9647746
99001 1161 1161 20318 20318 60442 60442 11252 11252 11252 1253 2533	ALIGNMENTS	chaffensi sion 21-A et, A.F.; ', 636-643 n of a.28	Score 79; Pred. No. ;; Mismatc 20	chaffensis sion 21-Au et, A.F.; , 636-643, on of a 28k
748901 748906 748161 748161 7402318 7480443 7480443 86606 86668 86668 86668 746644 74684 74684 74684	4	a cha visic rbet, 47, 6 ion c	(1)	a cha visic rbet, 47, 6
		chi re re re re re re re re re re re re re	8%; 7%; PILK	chie is rev Bar zati WID
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0.0000000		m 4 - MAP1 is a child	rity nser ?GLK	m 5 - MAP1 tia chi tia chi tia chi 8 8 8 8 8 8 8 8 8 8 9 9 9 9 9 9 9 9 9
4 4 4 4 4 4 4 4 M W W W W W W W W W W W		antigen names: h hrlichid ug-1998 Ug-1978 ; Sulsc phys. Re ecular: JE0217 ype: DW	Cor Cor Cor Cor Cor Cor	antigen names: N hrlichis ug-1998 JE0218 JE0218 cular o number: PE0218 YPE DNA
ক ক ক ক ক ক ক ক ল ল ল ল ল ল ল ল ক ক ক ক		ce ant: te name te name the name label lab	(f) st	face antigen nate names: des Ehrlichi, 21-Mug-1998 sion: JE0218 sion: JE0218 (G.R.; Bulghys. R. Molecular elone number: sion: JE0218 ule type: DM ues: 1-276
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Gaps

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ch 65.5%; Score 72; DB 2; Length 276; I Similarity 76.5%; Pred. No. 0.00081; 13; Conservative 2; Mismatches 2; Indels

Query Match Best Local Similarity Matches 13; Conserva

STVGVFGLKHDWDGSPI 18 TTVGVFGLKQNWDGSAI 76

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hypothetical prote protein W09G10.6 [2-demethylmenaquin hypothetical prote

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RESULT 3 140882

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E64142 B59103 T48902

A75466 D83445 G72596 AE3307

súlfate transporte

prote prote

hypothetical hypothetical

A.R.

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A;Map position: 5
A;Introns: 24/1; 245/3; 315/2; 389/3; 537/3; 568/2; 747/1
C;Superfamily: 6-phosphofructokinase, eukaryotic type; 6-phosphofructokinase 1 homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JE0221
28k surface antigen 2 - Ehrlichia canis
C;Species: Ehrlichia canis
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 21-Jul-2000
C;Accession: JE0221
K;Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem. Biophys Res. Comunn. 247, 636-643, 1998
A;Title: Molecular characterization of a 28kba surface antigen gene family of the tribe
A;Reference number: JE0216; MUID:98321180; PMID:9647746
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                                                                                                                                                                                                                                                                                                                                    whented to the EMBL Data Library, April 1996
A;Reference number: 219225
A;Reference number: 219225
A;Accession: 1720109
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Residues: 1-756 <WILL:
A;Coss-references: EMBL:270750; PIDN:CAA94737.1; GSPDB:GN00023; CESP:C50F4.2
A;Experimental source: clone C50F4
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                                                                                                                                                                                                     C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 12-May-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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A,Residues: 1-133 «RED»
A,Cross-references: GB:AF062762; NID:93327964; PIDN:AAC26722.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.7%; Score 47; DB 2; Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.5%; Score 50; DB 2; Length 756; 57.1%; Pred. No. 7.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                       hypothetical protein C50F4.2 - Caenorhabditis elegans
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Pred. No. 2.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
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Best Local Similarity 50.v.
3, Conservative
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nes 8; Conserv
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A;Gene: CESP:C50F4.2
                                                                                                                                                                                                                                                                              C, Accession: T20109
R; McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: JE0221
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Cispecies: Enrichia chaffensis
Cispecies: Enrichia chaffensis
Cipate: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 17-Mar-1999
Cipate: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 17-Mar-1999
Cipate: 21-Aug-1998 #sequence_revision 21-Aug-1998
Ricession: JE0219
A; Rederence number: JE0216; MUID:98321180; PMID:9647746
A; Reference number: JE0219
A; Reference number: DNA
A; Residues: 1-286 < RED>A; Residues: 1-286 < RED>A; Residues: 1-286 < RED>A; Residues: 1-286 < RED>A; Cross-references: GB:AF062761
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28k surface antigen 3 - Ehrlichia chaffensis
NyAlternate names: MAP1
Cispeciaes: Ehrlichia chaffensis
Cispeciaes: Disona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem: Biophys. Res. Commun. 247, 636-643, 1998
A;Fitle: Molecular characterization of a 28kDa surface antigen gene family of the tribe
A;Reference number: JE0216; MUID: 98321180; PMID: 9647746
A;Accession: UB0216
A;Molecule type: DNA
A;Residues: 1-278 ekED>
A;Cross-references: GB:AF062761
                                                                                                                                                                                                                                                gene encoding the
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major antigenic protein - heartwater rickettsia
C;Species: Cowdria ruminantium (heartwater rickettsia)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 08-Oct-1999
C;Accession: 140882; S42827
R;van Vliet, A.H.; Jongejan, F.; van Kleef, M.; van der Zeijst, B.A.
Infect. Immun. 62, 1451-1456, 1994
A;Title: Molecular cloning, sequence analysis, and expression of the gene enchance number: 140882; MUID:94178956; PMID:8132352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N;Alernate names: MAP1
C;Species: Ehrlichia chaffensis
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-284 <RES>
A;Cross-references: EMBL:X742SO; NID:g454266; PIDN:CAA52309.1; PID:g454267
C;Genetics:
A;Gene: mapl
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Pred. No. 0.14;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.2%; Score 53; DB 2; Length 278; 61.5%; Pred. No. 0.87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 58; DB 2; Length 284;
Pred. No. 0.14;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                       A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.7%;
66.7%;
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61 TTVGVFGIEQDWD 73
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62 TVALYGLKQDWEG 74
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Best Local Similarity
Local 9; Conserv?
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Matches 8; Conserv
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Matches 10; Conserv
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Cispecies: Pyrococcus abyssi
Cibate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
Cibate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
Rianonymous, Genoscope
Rianonymous, Genoscope
Aianonymous, Genoscope
Aibercription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str
Aireference number: A75001
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A;Molecule type: DNA
A;Residues: 1-103 <KAW>
A;Cross-references: GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB50524.1; PID:g54590
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                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:AF022967; PIDN:AAB69881.1; GSPDB:GN00023; CESP:C13A2.11
A;Experimental source: strain Bristol N2; clone C13A2
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A;Molecule type: DNA
A;Residues: 1-132 <KUR>
A;Cross-references: GB:BA000018; PID:g13700532; PIDN:BAB41829.1; GSPDB:GN00149
                                                      29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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A;Gene: PAB1286
C;Superfamily: Pyrococcus horikoshii hypothetical protein PH0346
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Pred. No. 5.6;
7; Mismatches 6; Indels
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                                                                              Cyaccession T32146
R;Rohlfing, T.; Wohldmann, P.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid C13A2.
A;Reference number: Z21126
A;Accession: T32146
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-231 <ROH>
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Pred. No. 11;
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28.6%;
                   C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence rev:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: CESP:C13A2.11
A;Map position: 5
A;Introns: 7/3; 33/3; 71/2; 219/1
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Best Local Similarity 35.0%;
Matches 7; Conservative
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Best Local Similarity 28.6
Matches 8; Conservative
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R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2322-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein Atu2284 [imported] - Agrobacterium tumefaciens (strain C5 C; Species: Agrobacterium tumefaciens (c) Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #sequence_revision 11-Jan-2002
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
Exage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein AGR_C_4151 [imported] - Agrobacterium tumefaciens (strain C58, Cere C; Species: Agrobacterium tumefaciens C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ster, E.W.
AyTitle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AÇ2857
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A;Experimental source: strain C58 (Dupont)
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hypothetical protein C13A2.11 - Caenorhabditis elegans
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16;
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           Pred. No. 12;
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A,Gene: Atu2284
A,Map position: circular chromosome
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148 LGLFGM--DWDSTPFL 161
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LGLFGM--DWDSTPFL 161
Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity
Matches 8; Conservat
                                                                                                                     HDWDGSPI 18
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Best Local Similarity
Matches 8; Conserv
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A;Molecule type: DNA
A;Residues: 1-385 <KUR>
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A; Residues: 1-385 < KUR>
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A;Gene: AGR
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5, 2003, 14:09:37

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46 KAQVGIVSM--DWDGNP 60
                                                                   Search completed: September
Job time : 42 secs
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Godon, J.J.; Chopin, M.C.; Ehrlich, S.D.
J. Bacteriol. 174, 6580-6589, 1992
A;Title: Branched-chain amino acid biosynthesis genes in Lactococcus lactis subsp. lacti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S35137
probable phosphogluconate dehydratase (EC 4.2.1.12) - Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Species: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: ilvD
C;Superfamily: dihydroxy-acid dehydratase
C;Keywords: branched-chain amino acid biosynthesis; carbon-oxygen lyase; hydro-lyase
                                                    A,Gene: tagD
C,Superfamily: Bacillus subtilis glycerol-3-phosphate cytidylyltransferase tagD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-570 <QQD>
A;Cross-references: EMBL:M90761; NID:g2565137; PIDN:AAB81918.1; PID:g2565156
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
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Pred. No. 19;
6; Mismatches
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                                                                                                                          Score 45; DB 2;
Pred. No. 7.3;
                                                                                                                                                                         2; Mismatches
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40.0%; Pred
6; F
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A, Experimental source: strain N315 C, Genetics:
                                                                                                                          Query Match
Best Local Similarity 53.3%;
Matches 8; Conservative 2
                                                                                                                                                                                                                                1 KSTVGVFGLKHDWDG 15
                                                                                                                                                                                                                                                          Conservative
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Best Local Similarity
Matches 8; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-311 <STO>
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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2003, 13:32:19; Search time 22 Seconds

(without alignments)

42.752 Million cell updates/sec
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Title: US-10-054-354-1
Perfect score: 110
Sequence: 1 KSTVGVFGLKHDWDGSPILK 20

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 127863 segs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIE

		Description .	caen	P55746 helicobacte		P20311 bacteriopha	_		P44509 haemophilus			O95167 homo sapien			_	P83119 drosophila			Q8txz9 methanopyru		homo		Q89al8 buchnera ap		-		P49026 nicotiana t			G		8 mycoplasm		118	Llan autlan coppon
SUMMARIES		ΙD	K6PF CAEEL	CGA2 HELPY	ILVD_LACLA	DPOL_BPT3	DPOL_BPT7	MENG_DEIRA	Y093 HAEIN	YABD_BACSU	CAGA_HELPY	NI 9M_HUMAN	NU2M_BOVIN	NU2M_HIPAM	NU2M_SHEEP	MTHC DROME	POLG PRSVH	YMSA RHIME	TRPF METKA	KC12 RAT	KC12_HUMAN	AT18_HUMAN	LIPB_BUCBP	TRPF_HALVO	CYSQ_ECOLI	GBLP_NICPL	GBLP_TOBAC	YA67_METTH						1	NET CHICK
		BB	н	~	Н	-	-	-	-	-	<b>,</b> -			Н	-1			-	-	-	-1		Н	Н	н	7	-	П	-	-	-	Н		-	
		Match Length	756	1182	570	704	704	160	368	255	1186	84	347	347	347	475	3344	102	216	414	415	1081	203	221	246	326	326	377	483	267	578	009	604	604	909
•	Query	Match	45.5	41.8	40.9	•	ö		40.0	39.1	σ	œ	œ	œ	38.2	38.2	œ	7	7	37.3	37.3	•	9	v	36.4	36.4	ဖ	v	ø	9	9	φ		36.4	36.4
		Score	20	46	45	45	45	44	44	43	4	42.5	42	42	42	42	42	41	41	41	41	41	40	40	40	40	40	40	40	40	40	40	40	40	40
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Q9pf41 xylella fas Q8pes0 xanthomonas	Q9plb0 chlamydia m P22925 petunia hyb	Q8ybp2 brucella me O8fwn5 brucella su	O9vpc0 drosophila	Q8ylk8 anabaena sp	O48650 salix bakko	Q8prx4 methanosarc	_	030207 archaeoglob
OSTA_XYLFA PLSB_XANAC	PMPD_CHLMU CHSD_PETHY	NAEK_BRUME NAEK_BRUSU	KP58_DROME	PAK2 ANASP	SUI1_SALBA	TRF2 METMA	YOAK BACSU	Y028_ARCFU
п п	~ ~		н	н	Н	-	ч	г
792 885	1520	518 525	952	92	113	226	284	371
36.4	36.4 35.9	35.9 35.9	35.9	35.5	35.5	35.5	35.5	35.5
4 4 0 0	40 39.5	39.5 39.5	39.5	39	39	39	39	39
3.4 3.5	36 37	38 36	40	41	42	43	44	45

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-fructose 1,6-bisphosphate.
-!- PATHMAX: Key control step of glycolysis.
-!- PATHMAX: Key control step of phosphofructokinase family. Two domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Probable 6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.5%; Score 50; DB 1; Length 756; 57.1%; Pred. No. 2.7; tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP, P00512; 3PFK.

WormPep, C50F4.2; CE05467.

WormPep, C50F4.2; CE05467.

InterPro: JPR00023; Ppfruckinase.

Pfam; PP00365; PFK; 2.

PRINTS; PR00476; PHFRCTKINASE.

PRODITE; PS00433; PHOSPHOFRUCTOKINASE; 1.

Kinase; Transferase; Glycolysis; Repeat.

SEQUENCE 756 AA; 83301 MW; 26A89B801D286534 CRC64;
                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z70750; CAA94737.1; -. PIR; T20109; T20109.
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Best Local Similarity 57.1
Matches 8; Conservative
                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                   (Phosphohexokinase).
C50F4.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=Bristol N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McMurray A.;
                                                                            CAEEL
RESULT 1
IN RESULT 1
IN CAREEL
IN OF 15-JUL
DT 15-JUL
DT 15-JUL
DT 15-SEP
DE PROBAD
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RESULT 2 CGA2_HELPY

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                                                                                                                                                                                                                                                                                                                                                                                                                              60737 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KSTVGVFGLKHDWDGSP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 KAQVGIVSM--DWDGNP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

Query Match

Best Local Similarity 47.11,

Best Local Similarity 67.11,
                                                                                                                                                                                                                                                                                                                                        4Fe-4S; Complete proteome.
                                                                                                                                                                                             EMBL; U92974; AAB81918.1;
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179
246
313
530
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179 1
246 2
313 3
530 5
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P20311;
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CONFLICT
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                                                                                                                                                             Tummaru M.K.R., Cover T.L., Blaser M.J.;
"Cloning and expression of a high-molecular-mass major antigen of "Helicobacter pylori: evidence of linkage to cytotoxin production.";
Infect. Immun. 61:1799-1809(1993).
-!- FUNCTION: MAY BE NECESSARY FOR THE TRANSCRIPTION, FOLDING, EXPORT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=NCDO 2118;
MEDI-INE=93015710; PubMed=1400210;
Godon J.-J., Chopin M.-C., Ehrlich S.D.;
"Branched-chain amino acid biosynthesis genes in Lactococcus lactis
                                                                          Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                              01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Cytotoxicity associated immunodominant antigen (120 kDa protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
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Pred. No. 19;
2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                         1182 AA; 131503 MW; C916817E2EE57BB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      570 AA.
 PRT; 1182 AA
                                                                                                                                                                                                                                                                                                                                                                                               POLY-ASN
                                                                                                                                                                                                                                                                                                                              EMBL; L11714; -; NOT_ANNOTATED_CDS.
INTERPRO; PRR005159; CagA.
InterPro; IPR004155; IVSec_cagA.
Pfam; PF03507; CagA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=1L1403;
MEDLINE=21235186; PubMed=11337471;
                                                                                                                                                                                                                    OR FUNCTION OF THE CYTOTOXIN.
                                                                                                                                                     MEDLINE=93239281; PubMed=8478069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriol. 174:6580-6589(1992)
                    (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR01553; TYPE4SSCAGA.
                                                                                                                                                                                                                                                                                                                                                                                                                               41.8%;
                                                                                                                             SEQUENCE FROM N.A. STRAIN=ATCC 53726 / 84-183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | || |||| |||| : :
323 GGFGAKHDWNAT 334
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 58.3
les 7; Conservative
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STANDARD;
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                                                                                                           NCBI_TaxID=210;
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Q02139;
                                                                 CAGA OR CAI
 HELPY
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Matches
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MEDLINES-9013922; PubMed=2614843;

MEDLINES-9013922; PubMed=2614843;

Bock P.J., Gonzalez S., Ward C.L., Molineux I.J.;

Bock P.J., Gonzalez S., Ward C.L., Molineux I.J.;

Sequence of bacteriophage T3 DNA from gene 2.5 through gene 9.";

J. Mol. Biol. 210:697-701(1989).

I. MOL. Biol. 210:697-701(1989).

EXHIBITS A 3 TO 5' EXONUCIBASE ACTIVITY.

-: CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus
lactis spp. lactis IL14403.";
Genome Res. 11.731-753 (2001).
-!- CATALYTIC ACTIVITY: 2,3-dihydroxy-3-methylbutanoate = 3-methyl-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAMAP, MF 00012; -; 1.

InterPro; IPR004404; IlvD.

InterPro; PR000361; ILvD. EDD_family.

Propon; PF0002691; ILVD EDD_family.

Propon; PF0002691; ILVD EDD_family; 1.

PROSITE; PF000887; ILVD EDD_1; 1.

PROSITE; PF00887; ILVD EDD_2; 1.

Branched-chain amino acid biosynthesis; Lyase; Iron; Iron-sulfur;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IRON-SULFUR (4FE-4S) (POTENTIAL).
IRON-SULFUR (4FE-4S) (POTENTIAL).
QDP -> PRG (IN REF. 1).
S -> A (IN REF. 1).
E -> D (IN REF. 1).
T -> I (IN REF. 1).
D -> N (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriophage T3.
Viruses, dsDNA viruses, no RNA stage, Caudovirales, Podoviridae,
T7-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                 oxobutanoate + H(2)O.
--- CORACTOR: BINDS I 4FE-4S CLUSTER (POTENTIAL).
--- PATHWAY: Valine and isoleucine biosynthesis; fourth step.
--- SIMILARITY: BELONGS TO THE ILVD / EDD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45; DB 1; Length 570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
08-FEB-2003 (Rel. 41, Last annotation update)
DNA polymerase (EC 2.7.7.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       704 AA
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SUBUNIT: COMPOSED OF TWO SUBUNITS. ONE IS ENCODED BY THE PHAGE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1299;
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MENG OR DR0859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                        DEIRA
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ID MENG_DEI
AC Q9RWI0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 391:251-258(1998).
-!- FUNCTION: IN ADDITION TO POLYMERASE ACTIVITY, THIS DNA POLYMERASE
EXHIBITS A 3' TO 5' EXONUCLEASE ACTIVITY.
-!- CAȚALYȚIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
             ENCODED BY THE PHAGE AND
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDILINE=89101638; PubMed=940688;
Doublie S., Tabor S., Long 4.0688;
"Crystal structure of a bacteriophage T7 DNA replication complex at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
T7-like viruses.
                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=83241725; PubMed=6864790;
Dunn J.J., Studier F.W.;
"Complete nucleotide sequence of bacteriophage T7 DNA and the locations of T7 genetic elements.";
J. Mol. Biol. 166:477-535(1983).
 + {DNA} (N).
-!- SUBUNIT: COMPOSED OF TWO SUBUNITS. ONE IS ENCODED BY THE THE OTHER IS ENCODED BY THE HOST THIOREDOXIN.
-!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                       InterPro; IPR001098; DNA pol.
InterPro; IPR002298; DNA_Doll.
InterPro; IPR00476; DNA_Doll.
PRIMTS; PR00486; DNA_DOLLA; 1.
PROSTITS; PS00447; DOLAC; I.
PROSTITE; PS00447; DNA_POLYMERASE A; 1.
Transferase; DNA-directed DNA_DOLYMERASE; DNA_POLYMERASE A; 1.
DNA-binding; Hydrolase; Exonuclease.
SEQUENCE 704 AA; 79985 MW; D65DFBD99AE31234 CRC64;
                                                                                                                                                                                                                                                                                                                 Length 704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=84164887; PubMed=6708104;
Moffatt B.A., Dunn J.J., Studier F.W.;
"Nucleotide sequence of the gene for bacteriophage T7 RNA
                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Last annotation update)
DNA polymerase (EC 2.7.7.7) (T7 DNA polymerase).
                                                                                                                                                                                                                                                                                                                 Score 45; DB 1;
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  704 AA.
                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polymerase.";
J. Mol. Biol. 173:265-269(1984).
                                                                                                                                                                                                                                                                                                                 40.9%;
                                                                                                                                                      EMBL; X17255; CAA35140.1; -. PIR; S07512; S07512.
                                                                                                                                                                                                                                                                                                                                         7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                      637 GLKHGWDG 644
                                                                                                                                                                                                                                                                                                                                                                8 GLKHDWDG 15
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                                                                                                                                                                              HSSP; P00581; 1T7P
                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10760;
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(DNA) (N)
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21-JUL-1986
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                                                                                                                                                                                                                                                                                                                 Query Match
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Matches
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                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensealsb-sib.ch).
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable S-adenosylmethionine:2-demethylmenaquinone methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSTITE: PS00447; DNA POLYMERASE A; 1.
Transferase, DNA-directed DNA polymerase; DNA replication; Hydrolase; Exonuclease; DNA-binding; 3D-structure.
SEQUENCE 704 AA; 79691 MW; 17089CE2AD9FB596 CRC64;
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MEDLINE=20036896; PubMed=10567266;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gavinn M.L., Nelson W.C., Richardson D.L.,
Noffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 286:1571-1577(1999).
-!- FUNCTION: CONVERTS DIMETHYLMENAQUINONE (DMK) TO MENAQUINONE (MK)
-|- EQU similarity:
-!- PATHWAY: Menaquinone blosynthesis; last step.
-!- SIMILARITY: BELONGS TO THE MENG FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.", % \left( \frac{1}{2}\right) =\frac{1}{2}\left( \frac{1}{2}
THE OTHER IS ENCODED BY THE HOST THIOREDOXIN. SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 45; DB 1; Length 704;
Pred. No. 16;
0; Mismatches 1; Indels
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Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 AA.
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PDB; JTTP; 25-EBB-98.
InterPro; IPR001099; DNA pol.
InterPro; IPR002298; DNA_pol.
Pfam; PF00476; DNA_pol A; 1.
PRINTS; PR00468; DNAPOLI.
SMART; SM00482; POLAG; 1.
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Best Local Similarity 87.2...
An Conservative
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or send an email to license@isb-sib.ch)

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STRAIN=168;
                               YABD BACSU
ID YABD BACSU
                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907;
STRAIN=Rd / KW20 / ATCC 51907;
STRAIN=Rd / KW20 / ATCC 51907;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Socott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.E., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hannam M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehn C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 368;
                                                                                                                                   Length 160;
                                                    HAMAP; MF 00471; -; 1.
InterPro; IPR005493; Methyltransf 6.
Pfam; PF03737; Methyltransf 6; 1.
Menaquinone biosynthesis; Transferase; Methyltransferase;
                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l protein; Complete proteome.
368 AA; 42251 MW; C77F1C9EF043B89A CRC64;
                                                                                                             160 AA; 16860 MW; 54D6F226CA19EC0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44; DB 1;
Pred. No. 12;
3; Mismatches
                                                                                                                                    Score 44; DB 1;
                                                                                                                                                                                                                                                                                            (Rel. 32, Last sequence update) (Rel. 41, Last annotation update)
                                                                                                                                                Pred. No. 5.1;
                                                                                                                                                                                                                                                              368 AA
                                                                                                                                                          5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 269:496-512(1995).
-!- SIMILARITY: BELONGS TO THE CDAR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                  (Rel. 32, Created)
(Rel. 32, Last seq
                     EMBL; AE001940; AAF10437.1; -.
                                                                                                                                   40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U32695; AAC21771.1; -.
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                                                                                                                                                                                                                                                                                                                    Hypothetical protein HI0093.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 GLSHSWQGNELIK 295
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                                                                                                                                                           6; Conservative
                                                                                                                                                                                 4 VGVFGLKHDWDG 15
                                                                                                                                                                                             :||||::: |:|
79 LGVFGVENGWEG 90
                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                         Haemophilus influenzae.
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                                PIR, A75466; A75466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
wes 6; Conserv
                                                                                                                                                Local Similarity
                                                                                                   Complete proteome. SEQUENCE 160 AA;
                                                                                                                                                                                                                                                                                                                                                                           NCBI TaxID=727;
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                                             TIGR; DR0859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical
SEQUENCE 36
                                                                                                                                                                                                                                                                                   01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venter J.C.;
                                                                                                                                                                                                                                                                                            01-NOV-1995
28-FEB-2003
                                                                                                                                                                                                                                                            Y093 HAEIN
P44509;
                                                                                                                                   Query Match
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RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillet S., Bourshier L., Brans A., Braun M., Bignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Furington J.J., Pabret C., Ferrari E., Foulger B.A.,
RA Brissepi G., Exrington J., Fabret C., Ferrari E., Foulger D.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Muster M., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kurita K., Lopidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Kurita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Saco T., Scanlan E., Schleich S., Schroceter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Takeuchi M., Tanakoshi A., Taragai T., Takahashi H., Takemaru K.,
RA Takato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Winters P., Wabbat R., Yamamoto H., Yamane K., Yasauncto K., Yata K.,
RA Winters P., Wabbat R., Schroceter R., Washikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
R. T. The Complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. The restrictions on its was by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb.sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96051385; PubMed=7584024;
Ogasawara N., Nakai S., Yoshikawa H.;
"Systematic sequencing of the 180 kilobase region of the Bacillus
subtilis chromosome containing the replication origin.";
                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 390:249-256(1997).
-!- SIMILARITY: BELONGS TO THE TATD DNASE FAMILY.
                                                                                   01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putarive deoxyribonuclease yabb (EC 3.1.21.-)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98044033; PubMed=9384377;
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InterPro; IPR001130; TatD DNase.
Pfam; PF01026; TatD DNase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D26185; BAA05274.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z99104; CAB11815.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ONA Res. 1:1-14(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                              Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: MAY BE NECESSARY FOR THE TRANSCRIPTION, FOLDING, EXPORT, OR FUNCTION OF THE CYTOTOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Rleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness B.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey B.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Watdman J.M., Fujil C., Bowman C., Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
CCT-2001 (Rel. 40, Last annotation update)
(CAG pathogenicity island protein 26).
CAGA OR CAI OR CAG26 OR HP0547.
Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteria; Helicobacteraceae; Helicobacteria; Campylobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                           ö
              PROSITE; PS01137; TATD 1; 1.
PROSITE; PS01090; TATD 2; 1.
PROSITE; PS01091; TATD 3; 1.
Hypothetical protein; Hydrolase; Nuclease; Complete proteome. SEQUENCE 255 AA; 29232 MW; ADF8EE9F5AEB0ED4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1186;
                                                                                                                        39.1%; Score 43; DB 1; *Length 255; 50.0%; Pred. No. 12;
                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132386 MW; B05C3F2CCC4444F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 1;
Pred. No. 60;
                                                                                                                                                                                                                                                                                                                         PRT; 1186 AA.
                                                                                                                                                           Mismatches
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POLY-ASN.
                                                                                                                                           Pred.
TIGRFAMS; TIGRO0010; TIGR00010; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-26695 / ATCC 700392;
MEDLINE-97394467; PubMed-9252185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPRO05169; CagA.
InterPro; IPR004355; IVSec_cagA.
Efam; PF03507; CagA, IVSec_RRINTS; PR01553; TYPE4SSCAGA.
Antigen; Complete proteome.
                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE000569; AAD07614.1; -. PIR; C64588; C64588.
                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
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90 IGEMGLDYHWDKSP 103
                                                                                                                                                                                           4 VGVFGLKHDWDGSP 17
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                       STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 388:539-547(1997)
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                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=210;
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                                                                                                                                                                                                                                                                                                                       CAGA HELPY
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Gaps

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Indels

Mismatches

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Conservative

Best Local Similarity Matches 7; Conserv

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X Strausberg Room No. 1.

X Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

X Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

X A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haleh F.,

X A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

X Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,

R Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,

R Rohards S., Worley K.C., Hale S., Garcia A.M., Galve L., Hullyk S.W.,

RA Yillalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

R Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

R Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

R Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R Human and mouse conya sequences ".", An Anthon M. Smailus D.E.,

R Human and mouse conya sequences ".", An Anthon M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Blood; MEDIINE=20499367; PubMed=11042152; Zhang O.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G., Zhang O.-H., Ye M., Wu X.-Y., Ren S.-X., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W., Shen Y., Fun H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W., Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z., "Cloning and functional analysis of cDNAs with open reading frames for 300 previously undefined genes expressed in CD34+ hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!-: FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED TO BE UBIQUINONE.
                                                                                                                                                                                                          15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
MADH-ubiquinone oxidoreductase B9 subunit (EC 1.6.5.3) (EC 1.6.99.3)
(Complex I-B9) (CI-B9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-i- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
-i- SUBNUT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERRNT SUBNUTS.
-i- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99097250; PubMed=9878551; Loeffen J.L.C.M., Triepels R.H., van den Heuvel L., Schuelke M., Buskens C.A.F., Smeets R.J.P., Trijbels J.M.F., Smeitink J.A.M.; C. C.A.F., Smeets R.J.P., Trijbels J.M.F., Smeitink J.A.M.; C. C.DNA of eight nuclear encoded subunits of NDH:ubiquinone oxidoreductase: human complex I cDNA characterization completed."; Plochem. Biophys. Res. Commun. 253:415-422(1998).
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Res. 10:1546-1560(2000).
                                                                                                                                                                    STANDARD;
5 GVFGLKHDWDGS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stem/progenitor cells.";
                                           328 GGFGDKHDWNAT
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
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EMBL, AF490528; AAM08323.1; --
EMBL, AF490529; AAM08336.1; --
EMBL, AF493541; AAM12790.1; --
EMBL, AF493542; AAM12803.1; --
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ID NU2M_SHEEP
AC 078748;
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete sequence of bovine mitochondrial DNA. Conserved features of the mammalian mitochondrial genome."; J. Mol. Biol. 156:683-717(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-83010260; PubMed-7120390;
Anderson S., de Bruijn M.H.L., Coulson A.R., Eperon I.C., Sanger F.,
Young I.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=65, 66, D, and F;
Wettstein P.J.;
West raurus mitochondrial protein coding regions.";
Submitted (MAR-2002) to the EWBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                              MIM; 603832; -. GO; GO: C: NADH dehydrogenase complex (ubiquinone) (se. .. GO; GO: 0008137; F: NADH dehydrogenase (ubiquinone) activity; TAS. Oxidoreductase; Ubiquinone; NAD; Mitochondrion; Transmembrane. TRANSMEM 19 39 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUTAM BOVIN STANDARD; PRT; 347 AA.
P03892; Q8SFW9;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                   19 39 POTENTIAL.
84 AA; 9279 MW; 38B27A96D7A05D31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.6%; Score 42.5; DE
56.2%; Pred. No. 4.6;
tive 2; Mismatches
                                                                                                                                                                                      EMBL; AF044955; AAD05420.1; -.
                                                                                                                                                                                                                EMBL; AF070653; AAD20959.1; -. EMBL; BC022369; AAH22369.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 VGAF-LKNAWDKEPVL 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 VGVFGLKHDWDGSPIL 19
                                                                                                                                                                                                                                                               PIR; JE0379; JE0379.
Genew; HGNC:7686; NDUFA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99098146; PubMed=9881471;
Ursing B.M., Arnason U.;
Ursing B.M., Arnason U.;
"Analyses of mitochondrial genomes strongly support a hippopotamus-whale clade.";
Proc. R. Soc. Lond., B. Biol. Sci. 265:2251-2255(1998).
-! CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-! SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Hippopotamidae, Hippopotamus.
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PIR; A00415; QXBOZM.
InterPro; IPR001750; Oxidored_q1.
Pfam; PP00361; Oxidored_q1; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
VARIANT 227 227 T -> I (IN STRAIN F).
SEQUENCE 347 AA; 39254 MW; 24105538A1374585 CRC64;
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Pfam; PF00316; oxidored_q1; 1.
Oxidoreductase; NAD; Ubiquinne; Mitochondrion; Transmembrane.
SEQUENCE 347 A3, 38973 MW; B174E1D6B8EB7828 CRC64;
                                                                                                                                                                                             38.2%; Score 42; DB 1; Length 347; 38.9%; Pred. No. 24; tive 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
NADH-ubiquinone oxidoreductase chain 2 (RC 1.6.5.3).
Hippopotamus amphibius (Hippopotamus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.2%; Score 42; DB 1; 38.9%; Pred. No. 24;
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                                                                                                                                                                                                                                                                                                                                          223 STTTLSLSHTWNKTPIM 240
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                                                                                                                                                                            Query Match
Best Local Similarity 38.99
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Best Local Similarity
7; Conserve
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IDENTIFICATION
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TRANSMEM
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TRANSMEM
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  This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last amnotation update)
Probable G-protein-coupled receptor Mth-like 12 precursor (Methuselah-
                                                                                                                                                                                  "The complete mitochondrial DNA sequence of the domestic sheep (Ovis arise) and comparison with the other major ovine haplotype.";

"The comparison with the other major ovine haplotype.";

3. Mol. Evol. 47:44-448(1998)

-1. CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.

-1. SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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MEDLINE-20196066; PubMed=107311132;
MEDLINE-201960606; PubMed=107311132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Ovis.
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InterPro; IPR001750; Oxidored_q1.
InterPro; IPR001750; Oxidored_q1.
Pfam; PF00381; oxidored_q1; 1.
PRINTS; PR01436; NADHDHGNASE2.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
SEQUENCE 347 AA; 39128 MW; 5202DF0A0D6C991B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.2%; Score 42; DB 1; Length 347; 38.9%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Indels
   15-DEC-1998 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3).
MINDZ OR NDZ.
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                                                                                                                                                               STRAIN=Merinolandschaf; TISSUE=Liver; MEDLINE=98440761; PubMed=9767689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 38.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         like 12 protein).
MTHL12 OR MTH-LIKE-12.
                                                             Ovis aries (Sheep).
Mitochondrion.
                                                                                                                                                                                                                                                                  inner membrane
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                                                                                                                           NCBI TaxID=9940;
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Randon R.C., Roylesce X. Half, C., Blacel R.G., Changen C.R., Millos C.R., Abduyani A.A., An H.J., Andison C.R., Millos C.R., Abduyani A.A., An H.J., Andison C.R., Millos C.R., Abduyani A.A., Barendale J., Bayraktergoliu L., Beasloy E.M., Bancon C.B., Bartis R.C., Change E.M., Bancon C.B., Bartis R.C., Change E.M., Change E.M., Andison C.M., Bartis R.C., Changer C.M., Change E.M., Cha
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 41, Last annotation update)
Genome polyprotein (Contains N-terminal protein (Pl); Helper
component proteinase (EC 3.4.22.45) (HC-Pro); Protein P3; 6 kDa
protein 1 (KR1); Cytoplasmic inclusion protein (CI); 6 kDa protein 2
(KZ2); Genome-1linked protein (VPG); Nuclear inclusion protein A (NI-A)
(NIA) (EC 3.4.22.44) (49 kDa proteinase) (49 kDa-Pro); Nuclear
inclusion protein B (NI-B) (NIB) (RNA-directed RNA polymerase)
(EC 2.7.7.48); Coat protein (CP)].
Papaya ringspot virus (strain P) mutant HA).
Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang C.H., Bau H.J., Yeh S.D.; "Comparison of the nuclear inclusion b protein and coat protein genes of five papaya ringspot virus strains distinct in geographic origin and pathogenicity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=930900998; PubMed=1456896;
Wang C.H., Yeh S.D.;
"Nucleotide sequence comparison of the 3'-terminal regions of severe,
"nucleotide sequence comparison of the 3'-terminal regions of severe,
mild, and non-papaya infecting strains of papaya ringspot virus.";
Arch. Virol. 127:345-354 (1992).
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EXTRACELLULAR (POTENTIAL).

CYTOPLASUIC (POTENTIAL).

BY SIMILARITY.

BY SIMILARIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL). (POTENTIAL).
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(GLCNAC. .) (POTENTIAL)
(GLCNAC. .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3590FEF875F77264 CRC64;
EXTRACELLULAR (POTENTIAL)
                                                                                                                                              EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
                                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                         4 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
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J. Gen. Virol. 73:2531-2541(1992)
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TRANSMISSION AND ALSO HAS PROTECLYTIC ACTIVITY.
FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELLICASE ACTIVITY. IN MAY BE INVOLVED IN REPLICATION.
FUNCTION: WULLEAR INCLUSION PROTEIN A HAS PROTECLYTIC ACTIVITY.
CATALYTIC ACTIVITY: Hydrolyzes glutaminyl bonds, and activity is further restricted by preferences for the amino acids in P6 - P1' that vary with the species of potyvitus, e.g. Glu-Xaa-Xaa-Tyr-Xaa-Gln+(Ser or Gly) for the enzyme from tobacco etch virus. The natural substrate is the viral polyprotein, but other proteins and oligopeptides containing the appropriate consensus sequence are
                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: Hydrolyzes a Gly-|-Gly bond at its own C-
terminus, commonly in the sequence -Tyr-Xaa-Val-Gly-|-Gly, in the
processing of the potyviral polyprotein.

PTM: VEG IS COVALENTY LINKED TO THE GENOMIC RNA.

PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONL PROTEOLYTIC
PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
INDIVIDUAL PROTEINS.

SINILARITY: HE PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase, Transferase, Thiol protease, RNA-directed RNA polymerase, Coat protein, Polyprotein; Covalent protein-RNA linkage, Helicase, ATP-binding. 1 529 N-TERMINAL PROTEIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                      also cleaved.
CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 KDB PROTEIN 2 (BY SIMILARITY).
GENOWE-LINKED PROTEIN (BY SIMILARITY).
NUCLEAR INCLUSION PROTEIN A
NUCLEAR INCLUSION PROTEIN B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC INCLUSION PROTEIN (BY
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PROTEIN P3 (BY SIMILARITY)
6 KDa PROTEIN 1 (BY SIMILA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001650; Helicase_C.
InterPro; IPR001450; Peptidase_C4.
InterPro; IPR001456; Peptidase_C6.
InterPro; IPR001592; Poty coat.
InterPro; IPR001592; Poty Poty InterPro; IPR0015940; Poty Poty InterPro; IPR001205; RNA_D01_DS_FS.
InterPro; IPR001205; RNA_D01_PSVir.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00271; helicase Č; 1.
Pfam; PF00863; Peptidase C4; 1.
Pfam; PF00863; Peptidase C6; 1.
Pfam; PF00767; Poty.coat; 1.
Pfam; PF00680; NNA dep RNA pol; 1.
PRINTS; PR00966; NIAPOTYPTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; S4672; AAB23789.1; -.
EMBL; X67672; CAA47904.1; -.
PIR, JQ1899; JQ1899.
MEROPS; C04.009; -.
MEROPS; C06.001; -.
MEROPS; S30.001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X67673; CAA47905.1; -.
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SM00490; HELICC; 1
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InterPro; IPR001650; H
InterPro; IPR001730; P
InterPro; IPR001456; P
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CHAIN

(BY SIMILARITY).

2156 2156 COAT PROTEIN (BY SIMILARITY).

2156 2156 CONALENT LINKAGE OF VIRAL RNA (BY SIMILARITY).

1486 1493 ATP (POTENTIAL).

3344 AA; 381040 MW; E90CD7523AC5243D CRC64; NP BIND SEQUENCE CHAIN BINDING FT FT FT SO

0; Gaps Score 42; DB 1; Length 3344; Pred. No. 2.6e+02; 2; Mismatches 3; Indels Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative

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8 GLKHDWDGSPILK 20 ||| |||| ::| 2049 GLKGVWDGSLMIK 2061

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Search completed: September 5, 2003, 14:07:07 Job time : 23 secs

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